

FIGURE 1A

ATGGAGAGCAAGGTGCTGCTGGCCGTCGCCCTGTGGCTCTGCGTGGAGACCC
 GGGCCGCCTCTGTGGGTTTGCTAGTGTTTCTCTTGATCTGCCAGGCTCAGCA
 TACAAAAAGACATACTTACAATTAAGGCTAATACTCTTCAAATTACTTGAG
 GGGACAGAGGGACTTGACTGGCTTTGGCCCAATAATCAGAGTGGCAGTGAG
 CAAAGGGTGGAGGTGACTGAGTGCAGCGATGGCCTCTTCTGTAAGACACTCAC
 AATTCCAAAAGTGATCGGAAATGACACTGGAGCCTACAAGTGCTTCTACCGGG
 AAAGTACTTGGCCTCGGTCAATTTATGTCTATGTTCAAGATTACAGATCTCCATT
 TATTGCTTCTGTTAGTGACCAACATGGAGTCGTGTACATTACTGAGAACAAAA
 CAAAAGTGTGGTGATTCCATGTCTCGGGTCCATTTCAAATCTCAACGTGTCACTT
 TGTGCAAGATAACCCAGAAAAGAGATTTGTTCTGATGGTAACAGAATTTCTTG
 GACAGCAAGAAGGGCTTTACTATTCCCAGCTACATGATCAGCTATGCTGGCATG
 GTCTTCTGTGAAGCAAAAATTAATGATGAAAGTTACAGTCTATTATGTACATAG
 TTGTCGTTGTAGGGTATAGGATTTATGATGTGGTTCTGAGTCCGTCTCATGGAA
 TTGAACTATCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAAGTGAAC
 TAAATGTGGGGATTGACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATA
 AGAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGGAGTGAGATGAAGAAA
 TTTTGTAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAAGGATTGTAC
 ACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTGAG
 GGTCCATGAAAAACCTTTTGTGCTTTTGGAGTGGCATGGAATCTCTGGTGGA
 AGCCACGGTGGGGGAGCGTGTGAGAATCCCTGCGAAGTACCTTGGTTACCCAC
 CCCCAGAAATAAAATGGTATAAAAATGGAATACCCCTTGAGTCCAATCACACAA
 TTAAAGCGGGGCATGTACTGACGATTATGGAAGTGAGTGAAAGACACAGGA
 AATTACACTGTACATCTTACCAATCCCATTTCAAAGGAGAAGCAGAGCCATGTG
 GTCTCTCTGGTTGTGTATGTCCACCCAGATTGGTGAGAAATCTCTAATCTCTC
 CTGTGGATTCTACAGTACGGCACCACTCAAACGCTGACATGTACGGTCTATG
 CCATTCTCCCCGCATCACATCCACTGGTATTGGCAGTTGGAGGAAGAGTGC
 GCCAACGAGCCCAGCCAAGCTGTCTCAGTGACAAACCCATACCTTGTGAAGA
 ATGGAGAAGTGTGGAGGACTTCCAGGGAGGAAATAAAATTGAAGTTAATAAAA
 ATCAATTTGCTCTAATTGAAGGAAAAAACAAACTGTAAGTACCTTGTATCCA
 AGCGGCAAATGTGTGAGCTTTGTACAAATGTGAAGCGGTCAACAAAGTCGGGA
 GAGGAGAGAGGGTGATCTCCTTCCACGTGACCAGGGGTCTGAAATTACTTTG
 CAACCTGACATGCAGCCCACTGAGCAGGAGAGCGTGTCTTTGTGGTGACCTGC
 AGACAGATCTACGTTTGAGAACCTCACATGGTACAAGCTTGGCCACAGCCTCT
 GCCAATCCATGTGGGAGAGTTGCCACACCTGTTTGCAAGAACTTGGATACTCT
 TTGGAAATTGAATGCCACCATGTTCTCTAATAGCACAAATGACATTTTGATCATG
 GAGCTTAAGAATGCATCCTTGCAGGACCAAGGAGACTATGTCTGCCTTGCTCAA
 GACAGGAAGACCAAGAAAAGACATTGCGTGGTCAGGCAGCTCACAGTCCTAGA
 GCGTGTGGCACCCACGATCACAGGAAACCTGGAGAATCAGACGACAAGTATTG
 GGGAAAGCATCGAAGTCTCATGCACGGCATCTGGGAATCCCCCTCCACAGATC
 ATGTGGTTTAAAGATAATGAGACCTTGTAGAAGACTCAGGCATTGTATTGAAG
 GATGGGAACCGGAACCTCACTATCCGCAGAGTGAGGAAGGAGGACGAAGGCC
 TCTACACCTGCCAGGCATGCAGTGTCTTGGCTGTGCAAAAGTGGAGGCATTTT
 TCATAATAGAAGGTGCCAGGAAAAGACGAACTTGGAAATCATTATTCTAGTAG
 GCACGGCGGTGATTGCCATGTTCTTCTGGCTACTTCTTGTGTCATCCTACGGA
 CCGTTAAGCGGGCCAATGGAGGGGAACTGAAGACAGGGTACCTGTCCATCGT
 CATGGACCCAGATGAACTCCCATTTGGATGAACATTGTGAACGACTGCCTTATGA
 TGCCAGCAAATGGGAATTTCCCAGAGACCGGCTGAAGCTAGGTAAGCCTCTTG
 GCCGTGGTGCCTTTGGCCAAGTGATTGAAGCAGATGCCTTGGGAATTGACAAG
 ACAGCAACTTGCAGGACAGTAGCAGTCAAAATGTTGAAAGAAGGAGCAACACA
 CAGTGAGCATCGAGCTCTCATGTCTGAACTCAAGATCCTCATTATATTGGTCA
 CCATCTCAATGTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAGGAGGGCCAC
 TCATGGTGATTGTGGAATTTGCAAAATTTGGAACCTGTCCACTTACCTGAGGA
 GCAAGAGAAATGAATTTGTCCCTACAAGACCAAGGGGCACGATTCCGTCAA
 GGGAAAGACTACGTTGGAGCAATCCCTGTGGATCTGAAACGGCGCTTGGACAG

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FIGURE 1B

CATCACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTTGTGGAGGAGAAGTCCC
TCAGTGATGTAGAAGAAGAGGAAGCTCCTGAAGATCTGTATAAGGACTTCCTG
ACCTTGGAGCATCTCATCTGTTACAGCTTCCAAGTGGCTAAGGGCATGGAGTTC
TTGGCATCGCGAAAGTGTATCCACAGGGACCTGGCGGCACGAAATATCCTCTT
ATCGGAGAAGAACGTGGTTAAAATCTGTGACTTTGGCTTGGCCCGGGATATTTA
TAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGAT
GGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCCAGAGTGACGTCTGGT
CTTTTGGTGTGTTTGGCTGTGGGAAATATTTTCTTAGGTGCTTCTCCATATCCTGG
GGTAAAGATTGATGAAGAATTTTGTAGGCGATTGAAAGAAGGAAGTGAATGA
GGGCCCCCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGG
CACGGGGAGCCCAGTCAGAGACCCACGTTTTTCAGAGTTGGTGGAAACATTTGGG
AAATCTCTTGCAAGCTAATGCTCAGCAGGATGGCAAAGACTACATTGTTCTTCC
GATATCAGAGACTTTGAGCATGGAAGAGGATTCTGGACTCTCTCTGCCTACCTC
ACCTGTTTCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCCATTATGA
CAACACAGCAGGAATCAGTCAGTATCTGCAGAACAGTAAGCGAAAGAGCCGGC
CTGTGAGTGTA AAAACATTTGAAGATATCCCGTTAGAAGAACCAGAAGTAAAG
TAATCCCAGATGACAACCAGACGGACAGTGGTATGGTTCTTGCCTCAGAAGAG
CTGAAAACCTTTGGAAGACAGAACCAAATTATCTCCATCTTTTGGTGGAAATGGTG
CCCAGCAAAAGCAGGGAGTCTGTGGCATCTGAAGGCTCAAACCAGACAAGCG
GCTACCAGTCCGGATATCACTCCGATGACACAGACACCACCGTGTACTCCAGT
GAGGAAGCAGAACTTTTAAAGCTGATAGAGATTGGAGTGCAAACCGGTAGCAC
AGCCCAGATTCTCCAGCCTGACTCGGGGACCACACTGAGCTCTCCTCCTGTTTA
A

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FIGURE 2

MESKVLVALWLCVETRAASVGLPSVSLDLPRLSIQKDILT IKANTTLQITCRGQR
DLDWLWPNNQSGSEQRVEVTECDGLFCKTLTIPKVIGNDTGAYKCFYRETDLAS
VIYVYVQDYRSPFIASVSDQHGVVYITENKNKT VVIPCLGSI SNLNVSLCARYPEKR
FVPDGNRISWDSKKGFTIPSYMISYAGMV FCEAKINDESYQSIMYTVVVVGYRIYDV
VLSPSHGIELSVGEKLV LNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQS
GSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGM
ESLVEATVGERVRIPAKYLGYPPEIKWYKNGIPLESNHTIKAGHVLTIMEV SERDT
GNYTVILTNPISKEKQSHVVS LVVYVPPQIGEKSLISP VDSYQYGT TQTLTCTVY AIP
PPHHHWHYWQLEEECANEPSQAVSVTNPYPC EEWRSVEDFQGGNKIEVNKNQFA
LIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPEITLQPD MQP
TEQESVSLWCTADRSTFENLTWYKLGPOPLPHV GELPTPVCKNLDTLWKL NATM
FSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHC VVRQLTVLERVAPTITGN
LENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRVRK
EDEGLYTCQACSVLGCAKVEAFFIEGAQ EKTNLEIILVGTAVIAMFFWLLLVIILRT
VKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRG
AFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVV
NLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFV PYKTKGARFRQGKD YVG
AIPVDLKRRLDSITSSQSSASSGFVEEKSLS DVEEEEAPEDLYKDFLTLEHLICYSFQ
VAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKG DAR
LPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGT
RMRAPDYTTPEMYQTMLDCWHGEP SQRPTFSELVEHLGNLLQANAQQDGKDYVL
PISETLSMEEDSGLSLPTSPVSCMEEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVS
VKTFEDIPLPEEVKVIPDDNQTD SGMVLA SEELKTLEDRTKLSPSFGGMVPSKSRE
SVASEGSNQTSGYQSGYHSDDTDTTVYSSEEAE LLKLEIGVQTGSTAQILQPDSGT
TLSSPPV

T0322F 6622001

FIGURE 3A

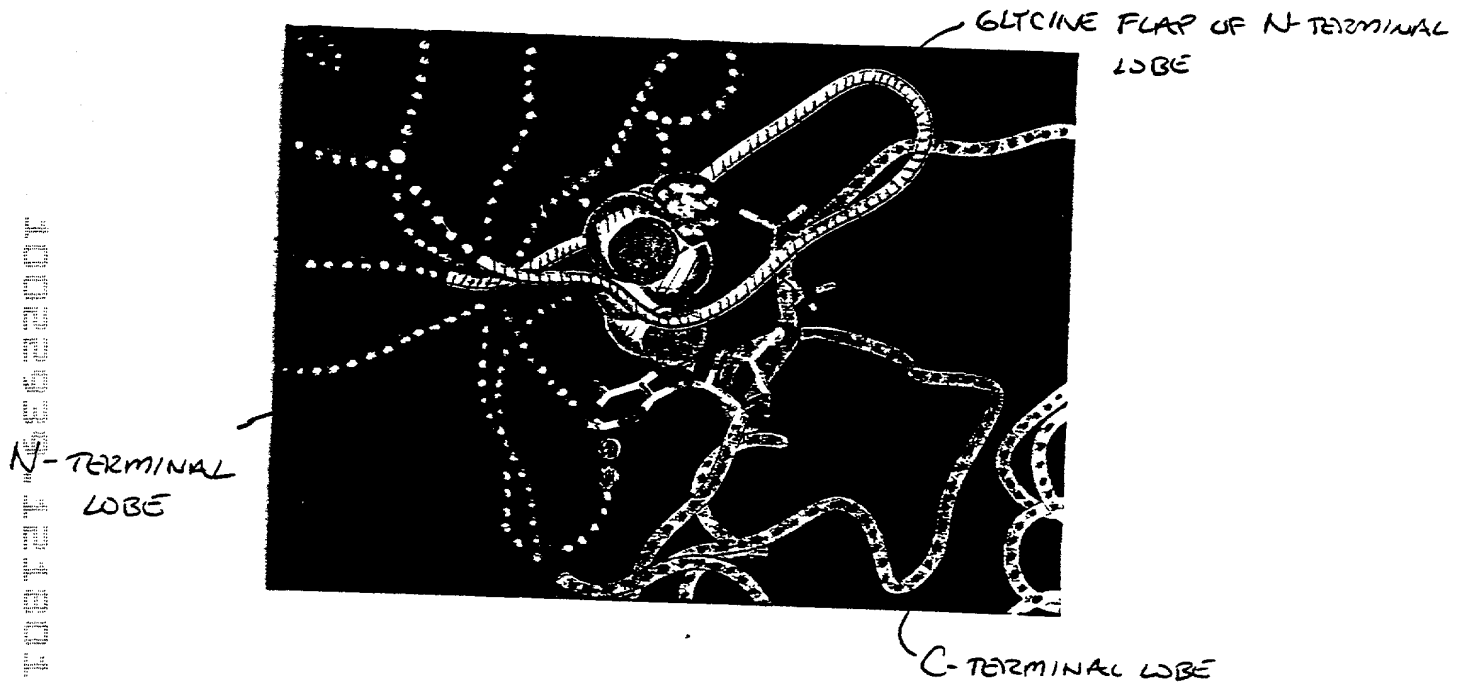


FIGURE 3B

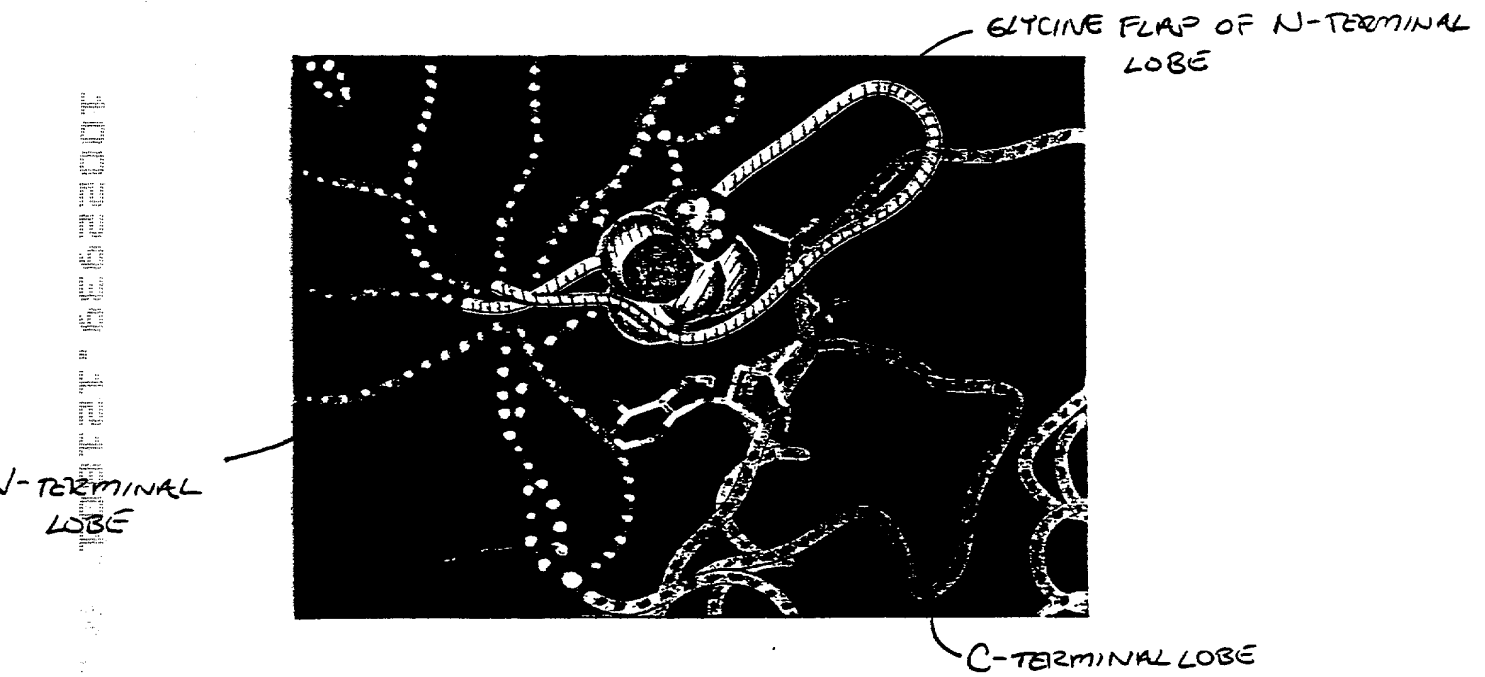


FIGURE 4A

Anti-phosphotyrosine

E848 **V848**

12	12	120	12	12
-	+	+	-	+

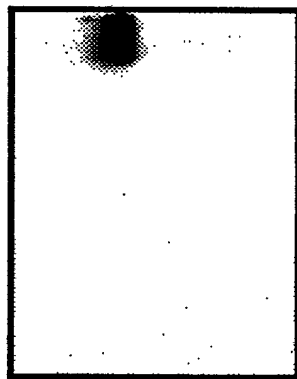


FIGURE 4B

Anti-KDR

E848 **V848**

120	12
-	-
Enzyme (ng)	
ATP (1 mM)	

